

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on : May 7, 2002, 11:58:52 ; Search time 26.38 Seconds

(without alignments)
190.229 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGQFRHKAQNLATRWW.....MPPTPECEKQFQPYFIPIN 223

Scoring table: Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

All number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/podata/2/iaa/5A_COMB_pep:*

2: /cgn2_6/podata/2/iaa/5B_COMB_pep:*

3: /cgn2_6/podata/2/iaa/6A_COMB_pep:*

4: /cgn2_6/podata/2/iaa/6B_COMB_pep:*

5: /cgn2_6/podata/2/iaa/pcrus_COMB_pep:*

6: /cgn2_6/podata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1158	91.6	223	3	US-08-228-208A-17	Sequence 17, Appl
2	1103.5	94.0	234	1	US-08-505-058-1	Sequence 1, Appl
3	1103.5	94.0	234	2	US-08-459-818-21	Sequence 21, Appl
4	1103.5	94.0	234	2	US-08-889-666-21	Sequence 21, Appl
5	1103.5	94.0	234	2	US-08-465-078-21	Sequence 21, Appl
6	1103.5	94.0	234	2	US-08-725-776-21	Sequence 21, Appl
7	1103.5	94.0	234	2	US-08-488-062-21	Sequence 21, Appl
8	970	82.6	187	1	US-08-067-684-14	Sequence 14, Appl
9	970	82.6	187	1	US-08-008-898-14	Sequence 14, Appl
10	970	82.6	187	2	US-08-459-818-14	Sequence 14, Appl
11	970	82.6	187	2	US-08-889-666-14	Sequence 14, Appl
12	970	82.6	187	2	US-08-465-078-14	Sequence 14, Appl
13	970	82.6	187	2	US-08-725-776-14	Sequence 14, Appl
14	970	82.6	187	2	US-08-458-062-14	Sequence 14, Appl
15	970	82.6	187	3	US-08-228-208A-14	Sequence 14, Appl
16	967	82.4	187	5	PCT-US95-06726-36	Sequence 36, Appl
17	857	73.0	223	3	US-08-228-208A-18	Sequence 18, Appl
18	804.5	68.5	234	1	US-08-505-058-2	Sequence 2, Appl
19	804.5	68.5	234	2	US-08-459-818-22	Sequence 22, Appl
20	804.5	68.5	234	2	US-08-889-666-22	Sequence 22, Appl
21	804.5	68.5	234	2	US-08-465-078-22	Sequence 22, Appl
22	804.5	68.5	234	2	US-08-725-776-22	Sequence 22, Appl
23	804.5	68.5	234	2	US-08-488-062-22	Sequence 22, Appl
24	648	55.2	124	4	US-08-530-072-4	Sequence 4, Appl
25	648	55.2	357	3	US-08-030-419-4	Sequence 4, Appl
26	648	55.2	357	4	US-09-375-419-20	Sequence 20, Appl
27	648	55.2	357	4	US-08-228-208A-17	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-228-208A-17

; Sequence 17, Application US/08228208A

; GENERAL INFORMATION:

; ; APPLICANT: Linsley, Peter S.

; ; ; PATENT NO. 609094

; ; ; ATTORNEY/AGENT INFORMATION:

; ; ; ; NAME: Adriano, Sarah B.

; ; ; ; REGISTRATION NUMBER: 34,470

; ; ; ; REFERENCE/DOCKET NUMBER: 30436-30US01

; ; ; ; TELECOMMUNICATION INFORMATION:

; ; ; ; TELEPHONE: 310 445-1140

; ; ; ; TELEFAX: 310 445-9031

; ; ; ; INFORMATION FOR SEQ ID NO: 17:

; ; ; ; SEQUENCE CHARACTERISTICS:

; ; ; ; LENGTH: 223 amino acids

; ; ; ; TYPE: amino acid

; ; ; ; STRANDEDNESS: unknown

; ; ; ; TOPOLOGY: linear

; ; ; ; MOLECULE TYPE: protein

; ; ; ; US-08-228-208A-17

QY 119 LRAMDTGLYICKVELMPPPYL-GIGNGAQIYVDPFPC----PDSDFLLWILAAVSS 172
 Db 121 LRAMDTGLYICKVELMPPPYL-GIGNGAQIYVDPFPCXXXPDSDFLWILAAVSS 180

QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTCGVYVKMPPECE-T-KQFQPFIFIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTCGVYVKMPPECEXXKQFQPFIFIN 234

RESULT 5
 US-08-465-078-21

Sequence 21 Application US/08465078
 Patent No. 5885796

GENERAL INFORMATION:
 APPLICANT: Linsley, Peter S.
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Damle, Nitin K.
 APPLICANT: Brady, William
 APPLICANT: Kienker, Peter A.

TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/465,078
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REFERENCE NUMBER: 34,470
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-465-078-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.4e-105;
 Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLNLAIRTPWTLFLFLFIPVCKAMHVQPAVVLASSRGIAFVCEY 60
 Db 1 MACLGFORHKAQNLNLAIRTPWTLFLFLFIPVCKAMHVQPAVVLASSRGIAFVCEY 60

QY 61 ASPGKATEVRVTVLROADSQTTECAATYMGNCNLFLDS--ICTGTSSGNQVNLTQG 118
 Db 61 ASPGKATEVRVTVLROADSQTTECAATYMGNCNLFLDSXXCTGTSSGNQVNLTQG 120

QY 119 LRAMDTGLYICKVELMPPPYL-GIGNGAQIYVDPFPC----PDSDFLLWILAAVSS 172
 Db 121 LRAMDTGLYICKVELMPPPYLXGIGNGTQIVYDPECPXXXPDSDFLWILAAVSS 180

QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTCGVYVKMPPECE-T-KQFQPFIFIN 223
 Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTCGVYVKMPPECEXXKQFQPFIFIN 234

RESULT 6 Sequence 21, Application US/08488062
 US-08-725-776-21 ; Patent No. 5977318
 ; Sequence 21, Application US/08725776
 ; Patent No. 5988510
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Damle, Nitin K.
 ; APPLICANT: Brady, William K.
 ; APPLICANT: Kiener, Peter A.
 ; TITLE OF INVENTION: CTA4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/725,776
 ; FILING DATE:
 ; PRIORITY APPLICATION NUMBER: US 08/375390
 ; CLASSIFICATION:
 ; APPLICATION NUMBER: US 08/375390
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adriano, Sarah B.
 ; REGISTRATION NUMBER: 34,470
 ; REFERENCE/DOCKET NUMBER: 30436-35US01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-445-1140
 ; TELEFAX: 310-445-9031
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-488-062-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
 Best Local Similarity 94.0%; Pred. No. 1.e-105; Gaps 5;
 Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKQNLNATRWPCTLFLFLPVECKAMHVQPAVVLASSRGIAASPVCEY 60
 Db 1 MACLGFORHKQNLNATRWPCTLFLFLPVECKAMHVQPAVVLASSRGIAASPVCEY 60
 QY 1 ASPGKATEVRVTLROADSQTTECATYMMGNELTPFLDDS - ICNTGSSGNQVNLTIG 118
 Db 1 ASPGKATEVRVTLROADSQTTECATYMMGNELTPFLDDS - ICNTGSSGNQVNLTIG 118
 QY 119 LRMDTGLYICKVELMPPPYL-GIGNGAQIVIDPEPC----PDSDFLWILAAVSS 172
 Db 119 LRMDTGLYICKVELMPPPYL-GIGNGAQIVIDPEPC----PDSDFLWILAAVSS 172
 QY 61 ASPGKATEVRVTLROADSQTTECATYMMGNELTPFLDDS - ICNTGSSGNQVNLTIG 118
 Db 61 ASPGKATEVRVTLROADSQTTECATYMMGNELTPFLDDS - ICNTGSSGNQVNLTIG 120
 QY 119 LRMDTGLYICKVELMPPPYL-GIGNGAQIVIDPEPC----PDSDFLWILAAVSS 172
 Db 121 LRMDTGLYICKVELMPPPYLXGNGTQIYVIDPEPCXXXPDSDFLWILAAVSS 180
 QY 173 GLFFYSFLLT-AVLSKMLKRSPLTTGVKMPTEPECE--KQFQYFIPIN 223
 Db 181 GLFFYSFLLTAVLSKMLKRSPLTTGVKMPTEPECEXXKQFQYFIPIN 234

RESULT 8
 US-08-067-684-14
 ; Sequence 14, Application US/08067684
 ; Patent No. 534431
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.

RESULT 7
 US-08-488-062-21

APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Suite 900
; CITY: Pasadena
; STATE: California
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/067,684
; FILING DATE: 26-MAY-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 7848-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310/312-9900
; FAX: 310/479-8340
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-067-684-14

Query Match 82.6%; Score 970; DB 1; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 0; Gaps 0;

QY 37 AMHQAPAVVLAASSRGIASTVCEASPGKATEEVRTVLROADSQTVECAATYMMGNELT 96
Db 1 AMHQAPAVVLAASSRGIASTVCEASPGKATEEVRTVLROADSQTVECAATYMMGNELT 60

QY 97 FLDDSICTGTSGNQNVLTIQGLRMTGTYICKVELMPPPYLIGNGAQIYVDPEP 156
Db 61 FLDDSICTGTSGNQNVLTIQGLRMTGTYICKVELMPPPYLIGNGQIYVDPEP 120

QY 157 CPDSDFLLWILAAVSSGLFFYSFLLTAWSKMLKKRSPLTGTVVKKMPTEPECEKQFQ 216
Db 121 CPDSDFLLWILAAVSSGLFFYSFLLTAWSKMLKKRSPLTGTVVKKMPTEPECEKQFQ 180

QY 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 10
US-08-459-818-14
; Sequence 14, Application US/08459818

RESULT 9
US-08-008-8198-14
; Sequence 14, Application US/08008898
; Patent No. 5,770,917

GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William K.
; APPLICANT: Gould, William K.
; APPLICANT: Nitin K.

CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FastSeq 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459, 818
 FILING DATE: 12-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-459-818-14

Query Match 82.6%; Score 970; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92; Indels 0; Gaps 0;
 Matches 186; Conservative 0; Mismatches 1; Insertions 0; Gaps 0;

QY 37 AMHVAQPAVLLAASSRGIAFSEYASPGKATEVRVTLRQADSQTEVCAATYMMGNELT 96
 Db 1 AMHVAQPAVLLAASSRGIAFSEYASPGKATEVRVTLRQADSQTEVCAATYMMGNELT 60

QY 97 FLDDSICGTSGSNQVNLTIGRAMDTGLYICKVELMPPYLYLGNGAGIYVIDPEP 156
 Db 61 FLDDSICGTSGSNQVNLTIGRAMDTGLYICKVELMPPYLYLGNGTQIYVIDPEP 120

QY 157 CPDSDFLWILAAVSSGLEFFYSFLLTAVSLSKMLKRSPLTGVYKMPTEPECEKQFQ 216
 Db 121 CPDSDFLWILAAVSSGLEFFYSFLLTAVSLSKMLKRSPLTGVYKMPTEPECEKQFQ 180

RESULT 12
 US-08-459-818-14
 Sequence 14, Application US/08465078
 ; Patent No. 5885796
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Danie, Nitin K.
 ; APPLICANT: Brady, William
 ; APPLICANT: Kienner, Peter A.
 ; TITLE OF INVENTION: CTP4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/465, 078
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/375390
 ; FILING DATE: 18-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; CLASSIFICATION: 435

RESULT 11
 US-08-459-666-14
 Sequence 14, Application US/088889666
 ; Patent No. 5885579
 ; GENERAL INFORMATION:
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Danie, Nitin K.
 ; APPLICANT: Brady, William
 ; APPLICANT: Kienner, Peter A.
 ; TITLE OF INVENTION: CTP4 Receptor and Uses Thereof
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/889, 666
 ; FILING DATE: 08-JUL-1997
 ; CLASSIFICATION:

NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-465-078-14

Query Match Score 970; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 0; Gaps 0;

37 AMHVAQPAVVLASSRGTSASFVCEYASPGKATEVRVTLROADSQTEVCATYMMGNELT 96
 1 AMHVAQPAVVLASSRGTSASFVCEYASPGKATEVRVTLROADSQTEVCATYMMGNELT 60

QY 97 FLDDSICGTGSSGNVNLTIGLKRMTGLICKVEMYPPPYLGNGAQIYVIDEP 156
 Db 61 FLDDSICGTGSSGNVNLTIGLKRMTGLICKVEMYPPPYLGNGTQIYVIDEP 120

QY 157 CPDSDFLWILAAVSSGLFFYSFLTLAVSLSKMLKRSPLTTGYYVMPPECEKQFQ 216
 Db 121 CPDSDFLWILAAVSSGLFFYSFLTLAVSLSKMLKRSPLTTGYYVMPPECEKQFQ 180

QY 217 PYFIPIN 223
 Db 181 PYFIPIN 187

RESULT 14
 US-08-488-062-14
 Sequence 14, Application US/08488062
 Patent No. 5977318

GENERAL INFORMATION:
 APPLICANT: Linsley, Peter S.
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Damle, Nitin K.
 APPLICANT: Brady, William
 APPLICANT: Kiener, Peter A.
 TITLE OF INVENTION: CTA4 Receptor and Uses Thereof
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/725,776
 FILING DATE:
 CLASSIFICATION:
 APPLICATION NUMBER: US/08/375390
 FILING DATE: 18-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140

SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-468-062-14

MOLECULE TYPE: protein
 US-08-228-208A-14

Query Match 82.6%; Score 970; DB 2; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 82.6%; Score 970; DB 3; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 82.6%; Score 970; DB 3; Length 187;
 Best Local Similarity 99.5%; Pred. No. 5.1e-92;
 Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 37 AMHYAQPAVVLASSRGASFVCEYASPGKATEVRVYLROADSQTEVCAATYMMGNELT 96
 Db 1 AMHYAQPAVVLASSRGASFVCEYASPGKATEVRVYLROADSQTEVCAATYMMGNELT 60

b 1 AMHYAQPAVVLASSRGASFVCEYASPGKATEVRVYLROADSQTEVCAATYMMGNELT 60

Qy 97 FLDDSICGTSGSNQVNLTIGRADMGLYCKVELMPPYYLGINQAAQIVYDPEP 156
 Db 61 FLDDSICGTSGSNQVNLTIGRADMGLYCKVELMPPYYLGINQIVYDPEP 120

b 61 FLDDSICGTSGSNQVNLTIGRADMGLYCKVELMPPYYLGINQIVYDPEP 120

Qy 157 CPDSDFLLWIAAVSSGLFFYSFLLTAVSLSKMLKRSPLTGVYVKMPPTEPECEKQFQ 216
 Db 121 CPDSDFLLWIAAVSSGLFFYSFLLTAVSLSKMLKRSPLTGVYVKMPPTEPECEKQFQ 180

b 157 CPDSDFLLWIAAVSSGLFFYSFLLTAVSLSKMLKRSPLTGVYVKMPPTEPECEKQFQ 180

Qy 121 PYFIPIN 223
 Db 181 PYFIPIN 187

Search completed: May 7, 2002, 12:01:21
 Job time: 149 sec

RESULT 15
 US-08-228-208A-14
 Sequence 14, Application US/08228208A
 Patent No. 6090914

GENERAL INFORMATION:
 APPLICANT: Linslsey, Peter S.
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Danile, Nitin K.
 APPLICANT: Brady, William
 APPLICANT: Wallace, Phillip M.

TITLE OF INVENTION: CTI4/CD2819 HYBRID FUSION
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 11150 Santa Monica Boulevard, Suite 400
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/228,208A
 FILING DATE: 15-APR-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/008,898
 FILING DATE: 22-JAN-1993
 APPLICATION NUMBER: 07/723,617
 FILING DATE: 27-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-30US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310 445-1140
 TELEFAX: 310 445-9031
 TELEX:

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Copyright (C) 1993 - 2000 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: May 7, 2002, 11:59:17 ; Search time 32.09 Seconds
 (without alignments)
 529,353 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGFQRHKAQNLNATRW.....MPPTEPECEKQQFQPYFIPIN 223

Scoring table: BL05UN62

Gapop 10.0 , Gapext 0.5

Ig

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1159	98.7	223	2	T09536		Cytotoxic T-lympho
2	997	84.9	223	2	I46696		CTLA-4 precursor -
3	978	82.6	186	2	S08614		cytotoxic T-lympho
4	878	74.8	223	2	A29063		cytotoxic T-lympho
5	211	18.0	221	2	S25168		CHT28 protein - ch
6	204	17.4	221	2	I46689		CD8 precursor - r
7	200	17.0	36	1	I84732		cytotoxic T-lympho
8	187	15.9	220	1	RWHU28		T-cell surface gly
9	174.5	14.9	173	2	I46197		cell surface prote
10	170	14.5	218	2	A43523		T-cell surface gly
11	158	13.5	218	2	S24413		T-cell surface gly
12	101	8.6	132	2	S38646		Ig kappa chain V
13	10.0	8.6	120	2	S46370		Ig kappa chain V
14	99	8.4	124	2	S40336		Ig kappa chain V-J
15	97	8.3	108	2	S30521		Ig kappa chain V
16	97	8.3	128	2	S46372		light chain var
17	94	8.0	117	2	S46371		Ig kappa chain V
18	93	7.9	132	2	S40334		Ig kappa chain - h
19	92	7.8	117	2	S41812		Ig kappa chain V
20	91	7.8	108	2	S34007		Ig kappa chain V
21	90.5	7.7	4391	2	A38096		perlecan precursor
22	90.5	7.7	108	2	S36277		Ig lambda chain V
23	90.5	7.7	123	2	S40338		Ig kappa chain - h
24	90	7.7	140	2	PL0013		Ig kappa chain pre
25	89.5	7.6	3707	2	S18252		heparan sulfate pr
26	89	7.6	125	2	S40333		Ig kappa chain V-J
27	88	7.5	573	2	S12358		Ig mu chain Precur
28	87.5	7.5	88	2	S34104		Ig kappa chain V
29	87.5	7.5	213	2	A21177		light chain pre

RESULT 2

I46696

CTLA-4 precursor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Accession: I46696

C;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole

T-cell surface gly	30	87	7.4	207	2	I50609
vascular cell adhe	31	87	7.4	739	2	J50675
Ig lambda chain V	32	86	7.3	120	2	S30525
Ig kappa chain V-J	33	86	7.3	125	2	S40349
inducible T-cell c	34	86	7.3	199	2	S78540
Ig kappa chain pre	35	86	7.3	234	2	S14237
vascular cell adhe	36	85	7.3	739	2	JN0581
protein serine/thr	37	85	7.3	598	2	T42070
Ig lambda chain V	38	85	7.2	111	2	S36281
Ig kappa chain V	39	85	7.2	112	2	PL0274
Ig kappa chain V-J	40	85	7.2	125	2	S40333
protein-tyrosine k	41	85	7.2	1367	2	A41228
Ig kappa chain V	42	84.5	7.2	105	2	S26338
Ig kappa chain V	43	84.5	7.2	124	2	S40338
Ig kappa chain V	44	84	7.2	111	2	S38497
Ig kappa chain V	45	84	7.2	112	2	H26317

ALIGNMENTS

RESULT 1	T09536	cytotoxic T-lymphocyte protein 4 - human
C;Species: Homo sapiens (man)		
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000		
C;Accession: T09536		
R;Harper, K.; Bazzano, C.; Rouvier, E.; Mattei, M.G.; Golstein, P.		
J; Immunol. 147, 1037-1044, 1991		
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m		
A;Reference number: I49845		
A;Accession: T09336		
A;Molecule type: mRNA		
A;Residues: 1-223 <HAD>		
A;Cross references: EMBL:LI5006; NID:9291928; PID:9291929		
C;Genetics:		
A;Gene: CTIA4		
A;Map Position: 2q33		
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology		
C;Keywords: T-cell; transmembrane protein		
C;KeyWords: T-cell; transmembrane protein		
Query Match 98.7%; Score 1159; Best Local Similarity 98.7%; Pred. No 4; Length 223; Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Qy	1 MACLGFFQRHKQAQLNLNATRTWPCTLLFLFLFTPVFCKAMHYAQPAVVLASSRGIASFVCEY 60
Db	1 MACLGFFQRHKQAQLNLNARTWPCTLLFLFLFTPVFCKAMHYAQPAVVLASSRGIASFVCEY 60	
Qy	61 ASPGATEEVTVTFLRQDSOTVEAATYMGNEITLQGLR 120	
Db	61 ASPGATEEVTVLRLRQDSOTVEAATYMGNEITLQGLR 120	
Qy	121 AMDTGLYICKVELMYPPYYLGIGNGAQIYVIDPPCPDSDFLMLIAVSSGLEFYSFL 180	
Db	121 AMDTGLYICKVELYPPYYLGIGNGAQIYVIDPPCPDSDFLMLIAVSSGLEFYSFL 180	
Qy	181 LTAVSLSKMLKKRSPLTIVVWVQKMPPTPECEKFQPFIPIN 223	
Db	181 LTAVSLSKMLKKRSPLTIVVWVQKMPPTPECEKFQPFIPIN 223	
RESULT 2		
C;Species: Oryctolagus cuniculus (domestic rabbit)		
C;Accession: I46696		
C;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole		

Page 2

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1174	100.0	223	1	CTL4_HUMAN	P16410	homo sapien
2	1010	86.0	223	1	CTL4_PIG	Q9myx7	sus scrofa
3	997	84.9	223	1	CTL4_RABBIT	P42072	oryctolagus
4	878	74.8	223	1	CTL4_MOUSE	P09793	mus musculus
5	211	18.0	221	1	CD28_CHICK	P31043	gallus gallus
6	204	17.4	221	1	CD28_RABBIT	P2069	oryctolagus
7	203	17.3	219	1	CD28_BOVINE	Q28071	bos taurus
8	187	15.9	220	1	CD28_HUMAN	P10147	homo sapien
9	170	14.5	218	1	CD28_MOUSE	P31041	mus musculus
10	156	13.3	218	1	CD28_RAT	P31042	rattus norvegicus
11	91	7.8	4393	1	PGBM_HUMAN	P88160	homo sapien
12	89.5	7.6	3707	1	PGBM_MOUSE	Q05793	mus musculus
13	87	7.4	739	1	VGR1_RAT	P29534	rattus norvegicus
14	86	7.3	739	1	VCA1_MOUSE	P29533	mus musculus
15	85	7.2	1356	1	VGR2_HUMAN	P05968	homo sapien
16	85	7.2	1367	1	VGR2_MOUSE	P25918	mus musculus
17	83	7.1	111	1	LV2D_HUMAN	P01704	homo sapien
18	83	7.1	111	1	LV2D_MOUSE	P01707	homo sapien
19	83	7.1	1343	1	VGR2_RAT	Q08775	rattus norvegicus
20	82	7.0	215	1	CIB2_HUMAN	Q60939	homo sapien
21	81.5	6.9	111	1	KV12_RABBIT	P24380	equine herpesvirus 1
22	81	6.9	111	1	KV1H_HUMAN	P01693	oryctolagus cuniculus
23	81	6.9	1897	1	PTPF_HUMAN	P10586	homo sapien
24	79.5	6.8	108	1	MOG_MOUSE	Q61885	mus musculus
25	79	6.7	108	1	KVK_MOUSE	P04945	mus musculus
26	79	6.7	552	1	VGLIE_HSVEL	P18552	equine herpesvirus 1
27	78.5	6.7	108	1	KV1H_HUMAN	P01690	homo sapien
28	78.5	6.7	345	1	OPCM_RAT	P32736	rattus norvegicus
29	78	6.6	485	1	SAHH_MESCR	P93253	mesembryontic virus
30	78	6.6	3038	1	TRIO_HUMAN	Q75962	homo sapien
31	77.5	6.6	226	1	C79A_HUMAN	P11912	homo sapien
32	77.5	6.6	345	1	OPCM_BOVINE	P11834	bos taurus
33	77.5	6.6	345	1	OPCM_HUMAN	Q14982	homo sapien

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

All number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1174	100.0	223	1	CTL4_HUMAN	P16410	homo sapien
2	1010	86.0	223	1	CTL4_PIG	Q9myx7	sus scrofa
3	997	84.9	223	1	CTL4_RABBIT	P42072	oryctolagus cuniculus
4	878	74.8	223	1	CTL4_MOUSE	P09793	mus musculus
5	211	18.0	221	1	CD28_CHICK	P31043	gallus gallus
6	204	17.4	221	1	CD28_RABBIT	P2069	oryctolagus cuniculus
7	203	17.3	219	1	CD28_BOVINE	Q28071	bos taurus
8	187	15.9	220	1	CD28_HUMAN	P10147	homo sapien
9	170	14.5	218	1	CD28_MOUSE	P31041	mus musculus
10	156	13.3	218	1	CD28_RAT	P31042	rattus norvegicus
11	91	7.8	4393	1	PGBM_HUMAN	P88160	homo sapien
12	89.5	7.6	3707	1	PGBM_MOUSE	Q05793	mus musculus
13	87	7.4	739	1	VCA1_RAT	P29534	rattus norvegicus
14	86	7.3	739	1	VCA1_MOUSE	P29533	mus musculus
15	85	7.2	1356	1	VGR2_HUMAN	P05968	homo sapien
16	85	7.2	1367	1	VGR2_MOUSE	P25918	mus musculus
17	83	7.1	111	1	LV2D_HUMAN	P01704	homo sapien
18	83	7.1	111	1	LV2D_MOUSE	P01707	homo sapien
19	83	7.1	1343	1	VGR2_RAT	Q08775	rattus norvegicus
20	82	7.0	215	1	CIB2_HUMAN	Q60939	homo sapien
21	81.5	6.9	111	1	KV12_RABBIT	P24380	equine herpesvirus 1
22	81	6.9	111	1	KV1H_HUMAN	P01693	oryctolagus cuniculus
23	81	6.9	1897	1	PTPF_HUMAN	P10586	homo sapien
24	79.5	6.8	108	1	MOG_MOUSE	Q61885	mus musculus
25	79	6.7	108	1	KVK_MOUSE	P04945	mus musculus
26	79	6.7	552	1	VGLIE_HSVEL	P18552	equine herpesvirus 1
27	78.5	6.7	108	1	KV1H_HUMAN	P01690	homo sapien
28	78.5	6.7	345	1	OPCM_RAT	P32736	rattus norvegicus
29	78	6.6	485	1	SAHH_MESCR	P93253	mesembryontic virus
30	78	6.6	3038	1	TRIO_HUMAN	Q75962	homo sapien
31	77.5	6.6	226	1	C79A_HUMAN	P11912	homo sapien
32	77.5	6.6	345	1	OPCM_BOVINE	P11834	bos taurus
33	77.5	6.6	345	1	OPCM_HUMAN	Q14982	homo sapien

ALIGNMENTS						
RESULT 1						
CTL4_HUMAN						
ID	CTL4_HUMAN					
AC	P16410;					
DT	01-AUG-1990 (Rel. 15, Created)					
DT	01-APR-1993 (Rel. 25, Last sequence update)					
DT	20-AUG-2001 (Rel. 40, Last annotation update)					
DE	CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE ASSOCIATED ANTIGEN 4) (CTLA-4) (CD152 ANTIGEN).					
DE	GN CTLA4 OR CD152.					
RA	Homo sapiens (Human).					
RA	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
RA	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE OF 1-37 FROM N.A.					
RX	MEDLINE-91318145; PubMed-1713603;					
RA	Harper K., Balzano C., Rouvier B., Mattei M.-G., Luciani M.F., Golstein P.;					
RA	SEQUENCE OF 38-223 FROM N.A.					
RC	TISSUE-Lymphocytes;					
RX	MBDLINE-89120925; PubMed-3220103;					
RA	"Human Ig superfamily CTLA-4" gene; chromosomal localization and identity of protein sequence between murine and human CTLA-4					
RT	cDNA sequence;					
RT	cytoplasmic domains";					
RL	Eur. J. Immunol. 18:1901-1905 (1988).					
RN	[3]					
RP	FUNCTION.					
RX	MEDLINE-91341416; PubMed-1714933;					
RA	Linsley P.S., Brady W., Urnes M., Gribsmaire L.S., Damle N.K., Ledbetter J.A., Leytze G.,					
RA	"CTLA-4 is a second receptor for the B cell activation antigen B7.";					
RL	J. Exp. Med. 174:561-569(1991).					
RN	[4]					
RP	STRUCTURE BY NMR OF 37-165.					
RX	MEDLINE-97372889; PubMed-9228944;					
RA	Metzler W.J.J., Bajgoric J., Fenderson W., Shaw S.Y., Constantine K.L., Naemura J., Leytze G.,					
RA	"Subcellular location of type I membrane protein."					
RT	"Solution structure of human CTLA-4 and delineation of a CD80/CD86 binding site conserved in CD28."					
RL	Nat. Struct. Biol. 4:527-531(1997).					
CC	-1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION.					
CC	CC-1- SUBCELLULAR LOCATION:					
CC	"Solution structure of human CTLA-4 and delineation of a CD80/CD86 binding site conserved in CD28."					
CC	"Subcellular location of type I membrane protein."					
CC	-1- TISSUE SPECIFICITY: CELL SURFACE OF ACTIVATED T-LYMPHOCYTES.					
CC	CC-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.					
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD152 entry;					
CC	WWW= http://www.ncbi.nlm.nih.gov/prow/od/cd152.htm .					
CC	WWW= http://www.ncbi.nlm.nih.gov/prow/od/cd152.htm .					

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; M74363; AAA52127; 1.;
EMBL; M37245; AAA52773; 1.;
EMBL; M37243; AAA52773; 1.; JOINED.
EMBL; M37244; AAA52773; 1.; JOINED.
PIR; S08614; S06614;
PDB; 1AH1; 15-APR-98.
MIM; 123890; ;
InterPro; IPR003596; Ig_V.
Immunoglobulin domain; T-cell; transmembrane; Glycoprotein; Signal; 3D structure.
KW SIGNAL 1 35 POTENTIAL.
KW CHAIN 36 223 CYTOTOXIC T-LYMPHOCYTE PROTEIN 4.
KW DOMAIN 36 161 EXTRACELLULAR (POTENTIAL).
KW TRANSMEM 162 187 POTENTIAL.
KW DOMAIN 188 223 CYTOPLASMIC (POTENTIAL).
KW DOMAIN 39 140 IG-LIKE V-TYPE DOMAIN.
FET DISULFID 58 129
FET DISULFID 85 103 N-LINKED '(GLCNAC, . . .)' (POTENTIAL).
FET CARBOHYD 113 113 MW; 7525D6B3E029BA CRCG4;
SO SEQUENCE 223 AA; 24526 MW;

Query Match :13..... Score 1174; DB 1; Length 223;

	Query Match	Best Local Similarity	Score 1010;	DB 1;	Length 223;	0;
	86.0%	85.2%	Score 1010;	DB 1;	Length 223;	0;
	86.0%	85.2%	Pred. No.	1.4e-86;		
	86.0%	85.2%	14.	Mismatches		
	86.0%	85.2%	14.	Indels		
	86.0%	85.2%	14.	gaps		

Matches	223: Conservative	QY	1 MACLGFORHKQAQLNIAATRWPCTLFFLFLIPVCKAMHVAOPAVLASSRGJASFYCEY 60	Db	1 MACLGFORHKQAQLNIAATRWPCTLFFLFLIPVCKAMHVAOPAVLASSRGJASFYCEY 60
			1 MACLGFORHKQAQLNIAATRWPCTLFFLFLIPVCKAMHVAOPAVLASSRGJASFYCEY 60		1 MACLGFORHKQAQLNIAATRWPCTLFFLFLIPVCKAMHVAOPAVLASSRGJASFYCEY 60
			61 ASPKATEVTVLROADSQTVECAATYMMGNELTFLDSICCTGTSSGNQNULTIQGLR 120		61 ASPKATEVTVLROADSQTVECAATYMMGNELTFLDSICCTGTSSGNQNULTIQGLR 120
		Qy	61 ASPKATEVTVLROADSQTVECAATYMMGNELTFLDSICCTGTSSGNQNULTIQGLR 120		61 ASPKATEVTVLROADSQTVECAATYMMGNELTFLDSICCTGTSSGNQNULTIQGLR 120
			61 ASGRATEVTVLROADSQTVECAATYMMGNELTFLDSICCTGTSSGNQNULTIQGLR 120		61 ASGRATEVTVLROADSQTVECAATYMMGNELTFLDSICCTGTSSGNQNULTIQGLR 120
			121 AMDTGLIICKVEMYMPYYLIGIGNAQIYVIDPECPDSDFLWILAYSSGLEFFYSFL 180		121 AMDTGLIICKVEMYMPYYLIGIGNAQIYVIDPECPDSDFLWILAYSSGLEFFYSFL 180
		Qy	121 AMDTGLIICKVEMYMPYYLIGIGNAQIYVIDPECPDSDFLWILAYSSGLEFFYSFL 180		121 AMDTGLIICKVEMYMPYYLIGIGNAQIYVIDPECPDSDFLWILAYSSGLEFFYSFL 180
			121 AMDTGLIICKVEMYMPYYLIGIGNAQIYVIDPECPDSDFLWILAYSSGLEFFYSFL 180		121 AMDTGLIICKVEMYMPYYLIGIGNAQIYVIDPECPDSDFLWILAYSSGLEFFYSFL 180
			181 LTAVSLSKMLKKRSPLTTGYVKMPPTEPECEKOFQPYFIPIN 223		181 LTAVSLSKMLKKRSPLTTGYVKMPPTEPECEKOFQPYFIPIN 223
			181 LTAVSLSKMLKKRSPLTTGYVKMPPTEPECEKOFQPYFIPIN 223		181 LTAVSLSKMLKKRSPLTTGYVKMPPTEPECEKOFQPYFIPIN 223

RESULT	2	3
CTL4_PIG	STANDARD;	PRT; 223 AA.
AC Q9YX7;		
DT 20-AUG-2001 (Rel. 40, Created)		(Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)		(Rel. 40, Last annotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)		CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 4) (CTLA-4).
GN CTLA4.		
OS Sus scrofa (Pig).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
NCBI_TaxID:9823;		
RN [1]		
RP SEQUENCE FROM N.A.		
RP Tachedjian M., Chaplin P.J., Scheerlinck J.-P.Y., Tennent J.M.; "Molecular characterization and phylogenetic analysis of porcine cytotoxic T-lymphocyte-associated antigen 4 (CTnA4)."; Submitted (2000) to the EMBL/GenBank/DBJ databases.		
RT -1 FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1		
RESULT	3	
CTL4_RABBIT	STANDARD;	PRT; 223 AA.
ID CP14_RABBIT		
AC P42072;		
DT 01-NOV-1995 (Rel. 32, Created)		
DT 01-NOV-1995 (Rel. 32, Last sequence update)		
DT 20-AUG-2001 (Rel. 40, Last annotation update)		
DE CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 4) (CTLA-4).		
GN CTLA4		
OS Oryctolagus cuniculus (Rabbit).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.		
NCBI_TaxID:9886;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=B/J X CHBB; HM; MEDLINE=95363949; PubMed=7642234;		
RC RX Isono T.; Seto A.; "Cloning and sequencing of the rabbit gene encoding T-cell co-stimulatory molecules." RT RT RT RT		

Copyright GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:00:52 ; Search time 54.19 Seconds
(without alignments)
601.933 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGFORHKQALNLAQRTW.....MPPTEPECEKQFQPYFFIPIN 223

Scoring table: BLOSUM62

Gapext 0.5

Searched: 473505 seqs, 146273329 residues

Actual number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	95.6	223	6 Q9BDN7	Q9bdn7 papio anubis
2	118	95.2	223	6 Q9BDC4	Q9bdc4 macaca mulatta
3	106	91.7	223	6 Q9BDP1	Q9bdp1 aotus trivirgatus
4	1034	88.1	223	6 Q9XTA1	Q9xta1 felis silvestris
5	1012	87.9	223	6 Q9TII02	Q9tii02 canis familiaris
6	1022	87.1	223	6 Q9KGP2	Q9kgp2 canis familiaris
7	1014	86.4	223	6 Q9XY7	Q9xy7 felis silvestris
8	1006	85.7	223	6 Q9NI86	Q9ni86 sus scrofa
9	997	84.9	223	6 Q9XSL1	Q9xsl1 canis familiaris
10	996	84.8	223	1 Q9JLV3	Q9jlv3 marmota monax
11	984	83.8	221	6 Q2B090	Q2b090 bos taurus
12	975	83.0	221	6 Q97631	Q97631 ovis aries
13	896	76.3	223	11 Q9ZB59	Q9zb59 rattus norvegicus
14	882	75.1	223	11 Q9QZZ7	Q9qzz7 mus musculus
15	592	50.4	137	4 Q9653	Q9653 homo sapiens
16	587	50.0	115	4 Q9BZK2	Q9bzk2 homo sapiens
17	534	45.5	174	11 Q9ZIA7	Q9zia7 rattus norvegicus
18	442	37.6	84	4 Q9UKN9	Q9ukn9 homo sapiens
19	252	21.5	68	11 Q99PF8	Q99pf8 crictetus

ALIGNMENTS

RESULT	1	Q9BDN7	ID	Q9BDN7	PRELIMINARY;	PRT;	223 AA.
		AC	Q9BDN7;	AC	Q9BDN7;	AC	Q9BDN7;
		DT	01-JUN-2001	DT	01-JUN-2001	DT	01-JUN-2001
			(TREMBBLEl. 17, Created)				(TREMBBLEl. 17, Last sequence update)
		DT	01-JUN-2001	DT	01-JUN-2001	DT	01-JUN-2001
			(TREMBBLEl. 17, Last annotation update)				
		DE	CD152. PROTEIN PRECURSOR.	DE	CD152. PROTEIN PRECURSOR.	DE	CD152. PROTEIN PRECURSOR.
		GN	CTLA-4.	GN	CTLA-4.	GN	CTLA-4.
		OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordata; Catarrhini; Cercopithecoidea; Cercopithecine; Papio.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordata; Catarrhini; Cercopithecoidea; Cercopithecine; Papio.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordata; Catarrhini; Cercopithecoidea; Cercopithecine; Papio.
		OX	NCBI_TaxID=9555;	OX	NCBI_TaxID=9555;	OX	NCBI_TaxID=9555;
		RN	[1]	RN	[1]	RN	[1]
		RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
		RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.; Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.	RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.; Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.	RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.; Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.
		RT		RT		RT	
		RL	Immunogenetics 0:0-0(2001); DR	RL	Immunogenetics 0:0-0(2001); DR	RL	Immunogenetics 0:0-0(2001); DR
		KW	EMBL; AF344838; AAC37534.1; -.	KW	EMBL; AF344838; AAC37534.1; -.	KW	EMBL; AF344838; AAC37534.1; -.
		FT	Conservative	FT	Mismatches	FT	Mismatches
		SIGNAL	5;	SIGNAL	5;	SIGNAL	5;
		SEQUENCE	223 AA;	SEQUENCE	223 AA;	SEQUENCE	223 AA;
			37		37		37
			POTENTIAL.		POTENTIAL.		POTENTIAL.
			EC18C279CCCC5668 CRC64;		EC18C279CCCC5668 CRC64;		EC18C279CCCC5668 CRC64;

Page 2

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on : May 7, 2002, 11:58:42 ; Search time 53.91 Seconds
(without alignments)
306.406 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 MACLGFORHKAQNLNATRTW MPPTEPECEKOFQPYFIPIN 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Actual number of hits satisfying chosen parameters: 522463

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : A_Geneseq_1101:*

1: /SIDS8/gcadata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcadata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcadata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS8/gcadata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS8/gcadata/geneseq/geneseqp/AA1984.DAT:*

6: /SIDS8/gcadata/geneseq/geneseqp/AA1985.DAT:*

7: /SIDS8/gcadata/geneseq/geneseqp/AA1986.DAT:*

8: /SIDS8/gcadata/geneseq/geneseqp/AA1987.DAT:*

9: /SIDS8/gcadata/geneseq/geneseqp/AA1988.DAT:*

10: /SIDS8/gcadata/geneseq/geneseqp/AA1989.DAT:*

11: /SIDS8/gcadata/geneseq/geneseqp/AA1990.DAT:*

12: /SIDS8/gcadata/geneseq/geneseqp/AA1991.DAT:*

13: /SIDS8/gcadata/geneseq/geneseqp/AA1992.DAT:*

14: /SIDS8/gcadata/geneseq/geneseqp/AA1993.DAT:*

15: /SIDS8/gcadata/geneseq/geneseqp/AA1994.DAT:*

16: /SIDS8/gcadata/geneseq/geneseqp/AA1995.DAT:*

17: /SIDS8/gcadata/geneseq/geneseqp/AA1996.DAT:*

18: /SIDS8/gcadata/geneseq/geneseqp/AA1997.DAT:*

19: /SIDS8/gcadata/geneseq/geneseqp/AA1998.DAT:*

20: /SIDS8/gcadata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS8/gcadata/geneseq/geneseqp/AA2000.DAT:*

22: /SIDS8/gcadata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

1 AAG66519 standard; Protein; 223 AA.
ID AAG66519
XX
AC AAG66519;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human CTLA4.
XX
KW Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4; immunosuppressive; immunomodulator; autotaxin; vaccine; antibody; T cell; humanised antibody; graft rejection; allergy.
XX
OS Homo sapiens.
PN WO200154732-A1.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02653.
XX
PR 27-JAN-2000; 2000US-0178473.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
PI O'Hara D, Hinton P,
XX
DR WPI; 2001-403195/52.
DR N-PSDB; AAH76437.
XX
PT Novel antibody-toxic group conjugate comprising an antibody that

ALIGNMENTS

No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	223	22 AAG66519	Human CTLA4, Homo
2	1170	99.7	223	21 AAY15129	Human CTLA4 proteo
3	1159	98.7	223	18 AAW25111	Soluble human CTLA
4	1159	98.7	223	22 AUU00687	Human CTLA4 proteo
5	1103.5	94.0	234	20 AAY41133	Human CTLA4 proteo
6	1034	88.1	223	20 AAY41084	Feline CTLA4 proteo
7	1022	87.1	223	20 AAY41083	Canine CTLA4 proteo
8	1015	86.5	223	21 AAY32287	Feline CTLA4-4
9	1005	86.5	223	21 AAY32280	Cat CTLA-4 receptor
10	1006	85.7	223	21 AAY15122	Porcine CTLA-4 sol
11	984.5	83.9	211	20 AAW87550	Human CTLA4 recepto

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	223	22 AAG66519	Human CTLA4, Homo
2	1170	99.7	223	21 AAY15129	Human CTLA4 proteo
3	1159	98.7	223	18 AAW25111	Soluble human CTLA
4	1159	98.7	223	22 AUU00687	Human CTLA4 proteo
5	1103.5	94.0	234	20 AAY41133	Human CTLA4 proteo
6	1034	88.1	223	20 AAY41084	Feline CTLA4 proteo
7	1022	87.1	223	20 AAY41083	Canine CTLA4 proteo
8	1015	86.5	223	21 AAY32287	Feline CTLA4-4
9	1005	86.5	223	21 AAY32280	Cat CTLA-4 receptor
10	1006	85.7	223	21 AAY15122	Porcine CTLA-4 sol
11	984.5	83.9	211	20 AAW87550	Human CTLA4 recepto

recognizes a molecule expressed only on activated T cells, useful for modulating immune response for treating autoimmune disorder, allergic response -

Example 3; Page 114-115; 123pp; English.

The invention relates to an antibody-toxic group conjugate comprising an antibody that specifically recognises a molecule expressed only on activated T cells, and a toxic group. The T cell molecule is preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4). The antibody of the invention is a humanised anti-CTLA4 antibody comprising a sequence of 128 or 142 amino acids fully defined in the specification. The antibody-toxic group conjugate is useful for modulating the immune response in subject suffering from a disorder or condition such as autoimmune disorder, immune response to a graft, allergic response or an immune response to a therapeutic protein. The antibody is also useful for research purposes, e.g., in staining and isolating CTLA4-bearing cells. The antibody is also useful for T-cell typing, for isolating specific IL-2 receptor bearing cells or fragments of the receptor for vaccine preparation, and for determining the effectiveness of an agent to down regulate CTLA4 activity. The present sequence is human CTLA4, which is bound by the antibody provided in the invention.

Sequence	223 AA:	Query Match	100.0%	Score	1174;	DB	22;	Length	223;
		Best Local Similarity	100.0%	Pred.	No.	3e-106;			
		Matches	223;	Mismatches	0;	Indels	0;	Gaps	
Y		1	MACLGPFQRHKQLNLAATRTWPCTLLFLLFIPYFCAMHVAQPAVVLASSRGIASFVCY	60					
o			maclgpfqrhkqlnlaatrtwpctllfllfipyfcamhvaqpaavllassrgiasfv	60					
Y		61	ASPGKATEVRVTVLIRQADSQVTEVCAATYMMGNELTFLDDSCITGGSSSNQVNLTIGER	120					
o			aspkgatervtvlirqadsqvtevcaatymmgneletflddscitggsssnqvnltigir	120					
Y		121	AMDTGLYICKVELMPPVYLGIGNGAQIVIDPECPDSDLFLWILAAVSSGLEFFYSFL	180					
b			amdtglyickvelmppvylgngaqividecpdSDLFLWILAAVSSGFLffysfl	180					
Y		181	LTAVSLSKMLKKRSPLTTGCVVYMRMPTEPECEKOFOPYFTPIN	223					
b			ltavslskmlkkrsplttgcvvymrmpftepecekofoypyftpin	223					

Homo sapiens .	Location/Qualifiers 1..37 /label= Signal_peptide
S	Key
X	Peptide
X	T
X	T
X	T
X	W09957266-A2.
X	11-NOV-1999.
D	30-APR-1999;
X	99WO-GB01350.

XX	PR	30-APR-1998;	98GB-0009280.
XX	PA	(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD	
XX	PI	Lechler IR,	Dorling A;
XX	WPI	2000-038815/03.	
XX	DR	N-PSDB; AAZ29001.	
XX	PT	Inhibiting T-cell mediated rejection of x	
XX	PS	Disclosure; Fig 15; 43pp; English.	
XX	CC	The present sequence is the human CTLA-4 xenodraft-specific immunosuppression. So the organ recipient preferentially binds its interaction with CD28 on recipient T-stimulatory signal 2 is blocked and the this sequence has an overall homology of	
XX	SQ	Sequence 223 AA;	
Query Match 99.7% Score 1170; Best Local Similarity 99.6%; Pred. No 7 Matches 222; Conservative 0; Mismatch 1	1	MACLGFORHKQLNIAATRTPCTPLLFFFLFIPVFCI 1 maclgfqrhkqqlnlaatrtwpctpllfllffipvfc	
Db 61 ASPGKATEVRVTVLRQADSQTEVCATACTMMGNEL 61 aspgkatevrvtvlgqadsqtevcatactmmgnel	61	AMDTGLTICKREVMPPPPYLGNGAQIVYDPE 121 amdtglyickrevmpppyylgngqivydppe	
Db 121 IAVSISKMLKKRSPLITGVYVVKMPTEPECEKF 121 itavsiskmkkrsplittgvykmpptepecef	121	IATVSIKMLKKRSPLITGVYVVKMPTEPECEKF 181 itavsiskmkkrsplittgvykmpptepecef	
Db 181 IATVSIKMLKKRSPLITGVYVVKMPTEPECEKF 181 itavsiskmkkrsplittgvykmpptepecef	181		
RESULT 3			
XX	ID	AAW25111 standard; protein; 223 AA.	
XX	AC	AAW25111;	
XX	DT	03-NOV-1997 (first entry)	
XX	DE	Soluble human CTLA4 mutant molecule reads	
XX	KW	CTLA4; mutant; soluble; CD80 antigen; sp	
XX	KW	T cell surface receptor; B7-1; antibody	
XX	KW	autoimmune disease; chronic inflammation	
XX	KW	graft versus host disease.	
OS Homo sapiens.			
XX	Key	Location/Qualifiers	
XX	FH	1..37	
FT	Peptide	/label= sig_peptide	
FT	Protein	38..234 /label= mat_protein	
FT	Region	62..67 /note= "CDR 1-like region	
FT	Region	86..90 /note= "CDR 2-like region	
FT	Region	132..139 /note= "CDR 3-like region	
FT			